

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT:

(A) NAME: Koninklijke Universiteit Nijmegen.
Afdeling tumorimmunologie

(B) STREET: Philips van Leydenlaan 25

(C) CITY: Nijmegen

10 (E) COUNTRY: Netherlands

(F) POSTAL CODE (ZIP): 6525 EX

(G) TELEPHONE: + 31 243 617 600

(H) TELEFAX: + 31 243 540 339

15

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

20

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(ii) TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING
DENDRITIC CELL-T CELL INTERACTION

25

(iii) NUMBER OF SEQUENCES: 2

(2) INFORMATION FOR SEQ ID NO:1:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1215 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

40

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

45

ATGAGTGACT CCAAGGAACC AAGACTGCAG CAGCTGGGCC TCCTGGAGGA GGAACAGCTG 60

AGAGGCCTTG GATTCCGACA GACTCGAGGA TACAAGAGCT TAGCAGGGTG TCTTGGCCAT 120

GGTCCCCTGG TGCTGCAACT CCTCTCCTT ACGCTCTTG CTGGGCTCCT TGTCCAAGTG 180

50

TCCAAGGTCC CCAGCTCCAT AAGTCAGGAA CAATCCAGGC AAGACGCGAT CTACCAGAAC 240

CTGACCCAGC TTAAAGCTGC AGTGGGTGAG CTCTCAGAGA AATCCAAGCT GCAGGAGATC 300

55

TACCAGGAGC TGACCCAGCT GAAGGCTGCA GTGGGTGAGC TTCCAGAGAA ATCTAAGCTG 360

CAGGAGATCT ACCAGGAGCT GACCCGGCTG AAGGCTGCAG TGGGTGAGCT TCCAGAGAAA 420
 TCTAAGCTGC AGGAGATCTA CCAGGAGCTG ACCTGGCTGA AGGCTGCAGT GGGTGAGCTT 480
 5 CCAGAGAAAT CTAAGATGCA GGAGATCTAC CAGGAGCTGA CTCGGCTGAA GGCTGCAGTG 540
 GGTGAGCTTC CAGAGAAATC TAAGCAGCAG GAGATCTACC AGGAGCTGAC CCGGCTGAAG 600
 10 GCTGCAGTGG GTGAGCTTCC AGAGAAATCT AAGCAGCAGG AGATCTACCA GGAGCTGACC 660
 CGGCTGAAGG CTGCAGTGGG TGAGCTTCCA GAGAAATCTA AGCAGCAGGA GATCTACCAG 720
 GAGCTGACCC AGCTGAAGGC TGCAGTGGAA CGCCTGTGCC ACCCCTGTCC CTGGGAATGG 780
 15 ACATTCTTCC AAGGAAACTG TTAATTCTATG TCTAACTCCC AGCGGAACTG GCACGACTCC 840
 ATCACCGCCT GCAAAGAAGT GGGGGCCAG CTCGTCGTAA TCAAAAGTGC TGAGGAGCAG 900
 20 AACTTCCTAC AGCTGCAGTC TTCCAGAAGT AACCGCTTCA CCTGGATGGG ACTTTCAGAT 960
 CTAAATCAGG AAGGCACGTG GCAATGGGTG GACGGCTCAC CTCTGTTGCC CAGCTTCAAG 1020
 CAGTATTGGA ACAGAGGAGA GCCCAACAAC GTTGGGGAGG AAGACTGCGC GGAATTTAGT 1080
 25 GGCAATGGCT GGAACGACGA CAAATGTAAT CTTGCCAAAT TCTGGATCTG CAAAAAGTCC 1140
 GCAGCCTCCT GCTCCAGGGA TGAAGAACAG TTTCTTTCTC CAGCCCCTGC CACCCCAAAC 1200
 30 CCCCTCCTG CGTAG 1215

2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 415 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

45 Met Ser Asp Ser Lys Glu Pro Arg Leu Gln Gln Leu Gly Leu Leu
 1 5 10 15
 Glu Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly
 20 25 30
 50 Tyr Lys Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu
 35 40 45
 Gln Leu Leu Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val
 55 60

Ser Lys Val Pro Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp
 65 70 75
 5 Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly Glu
 80 85 90
 Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr
 95 100 105
 10 Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu
 110 115 120
 Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly
 125 130 135
 15 Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu
 140 145 150
 Thr Trp Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys
 155 160 165
 20 Met Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val
 170 175 180
 25 Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu
 185 190 195
 Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser
 200 205 210
 30 Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala
 215 220 225
 Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln
 230 235 240
 35 Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu Cys His Pro
 245 250 255
 40 Cys Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met
 260 265 270
 Ser Asn Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys Lys
 275 280 285
 45 Glu Val Gly Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln
 290 295 300
 50 Asn Phe Leu Gln Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp
 305 310 315
 Met Gly Leu Ser Asp Leu Asn Gln Glu Gly Thr Trp Gln Trp Val
 320 325 330
 55

Asp Gly Ser Pro Leu Leu Pro Ser Phe Lys Gln Tyr Trp Asn Arg
335 340 345

5 Gly Glu Pro Asn Asn Val Gly Glu Glu Asp Cys Ala Glu Phe Ser
350 355 360

Gly Asn Gly Trp Asn Asp Asp Lys Cys Asn Leu Ala Lys Phe Trp
365 370 375

10 Ile Cys Lys Lys Ser Ala Ala Ser Cys Ser Arg Asp Glu Glu Gln
380 385 390

Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn Pro Pro Pro Ala *

15 395 400 404